SEQUENCE LISTING

<110> Myriad Genetics, Inc.
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<120> Protein-Protein Interactions

<130> P218-290-II

<150> US 60/259,572
<151> 2001-01-04

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<170> PatentIn version 3.0

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gagacataca gacaagaaag gcaaaatcac a atg gcc tcc acc aat gca gag 172
Met Ala Ser Thr Asn Ala Glu
1 5

agc cag ctc cag aga atc atc cga gac ttg caa gat tct gtg aca gaa 220
Ser Gln Leu Gln Arg Ile Ile Arg Asp Leu Gln Asp Ala Val Thr Glu
10 15 20

tta agc aaa gaa ttt cag gaa gca ggg gaa ccc atc agg gat gac agc 268
Leu Ser Lys Glu Phe Gln Glu Ala Gly Glu Pro Ile Thr Asp Asp Ser
25 30 35

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acc agc ttg cat aaa ttt tct tat aaa ctt gag tat ctc ctg caa ttt          316
Thr Ser Leu His Lys Phe Ser Tyr Lys Leu Glu Tyr Leu Leu Gln Phe
 40                  45                  50                  55

gat cag aaa gag aag gcc acc ctc ctg ggc aac aag aag gac tac tgg          364
Asp Gln Lys Glu Lys Ala Thr Leu Leu Gly Asn Lys Lys Asp Tyr Trp
                 60                  65                  70

gat tac ttc tgt gcc tgc ctg gcc aag gtg aaa gga gcc aat gat ggg          412
Asp Tyr Phe Cys Ala Cys Leu Ala Lys Val Lys Gly Ala Asn Asp Gly
             75                  80                  85

atc cgc ttt gtc aag tct atc tca gag ctc cga aca tcc ttg ggg aaa          460
Ile Arg Phe Val Lys Ser Ile Ser Glu Leu Arg Thr Ser Leu Gly Lys
         90                  95                 100

gga aga gca ttt att cgc tac tcc ttg gtg cac cag agg ttg gca gac          508
Gly Arg Ala Phe Ile Arg Tyr Ser Leu Val His Gln Arg Leu Ala Asp
    105                 110                 115

acc tta cag cag tgc ttc atg aac act aaa gtg acc agt gac tgg tac          556
Thr Leu Gln Gln Cys Phe Met Asn Thr Lys Val Thr Ser Asp Trp Tyr
120                 125                 130                 135

tat gca aga agc ccc ttt ctg cag cca aag ctg agc tcg gac att gtg          604
Tyr Ala Arg Ser Pro Phe Leu Gln Pro Lys Leu Ser Ser Asp Ile Val
                140                 145                 150

ggc caa ctc tat gag ctg act gag gtt cag ttt gac ctg gcg tcg agg          652
Gly Gln Leu Tyr Glu Leu Thr Glu Val Gln Phe Asp Leu Ala Ser Arg
            155                 160                 165

ggc ttt gac ttg gat gct gcc tgg cca aca ttt gcc agg agg acg ctg          700
Gly Phe Asp Leu Asp Ala Ala Trp Pro Thr Phe Ala Arg Arg Thr Leu
        170                 175                 180

acc act ggc tct tct gct tac ctg tgg aaa ccc cct agc cgc agc tcc          748
Thr Thr Gly Ser Ser Ala Tyr Leu Trp Lys Pro Pro Ser Arg Ser Ser
    185                 190                 195

agc atg agc agc agc ttg gtg agc agc tac ctg cag act caa gag atg gtg          796
Ser Met Ser Ser Ser Leu Val Ser Ser Tyr Leu Gln Thr Gln Glu Met Val
200                 205                 210                 215

tcc aac ttt gac ctg aac agc ccc cta aac aac gag gca ttg gag ggc          844
Ser Asn Phe Asp Leu Asn Ser Pro Leu Asn Asn Glu Ala Leu Glu Gly
                220                 225                 230

ttt gat gag atg cga cta gag ctg gac cag ttg gag gtg cgg gag aag          892
Phe Asp Glu Met Arg Leu Glu Leu Asp Gln Leu Glu Val Arg Glu Lys
            235                 240                 245

cag cta cgg gag cgc atg cag cag ctg gac aga gag aac cag gag ctg          940
Gln Leu Arg Glu Arg Met Gln Gln Leu Asp Arg Glu Asn Gln Glu Leu
        250                 255                 260

agg gca gct gtc agc cag caa ggg gag caa ctg cag aca gag agg gag          988
Arg Ala Ala Val Ser Gln Gln Gly Glu Gln Leu Gln Thr Glu Arg Glu
    265                 270                 275

agg ggg cgc act gca gag gag gac aac gtt cgc ctc act tgc ttg gta         1036
Arg Gly Arg Thr Ala Glu Glu Asp Asn Val Arg Leu Thr Cys Leu Val
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gct gag ttc cag aag cag tgg gag gtt act cag gct act cag aac act      1084
Ala Glu Leu Gln Lys Gln Trp Glu Val Thr Gln Ala Thr Gln Asn Thr
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gtg aag gag ctg cag aca tgc ctg cag ggc ctg gag cta gga gca gca      1132
Val Lys Glu Leu Gln Thr Cys Leu Gln Gly Leu Glu Leu Gly Ala Ala
            315                 320                 325

gag aag gag gag gac tac cac aca gcc ctg cgg cgg ctg gag tcc atg      1180
Glu Lys Glu Glu Asp Tyr His Thr Ala Leu Arg Arg Leu Glu Ser Met
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ctg cag ccc ttg gca cag gag ctt gag gcc aca cgg gac tca ctg gac      1228
Leu Gln Pro Leu Ala Gln Glu Leu Glu Ala Thr Arg Asp Ser Leu Asp
    345                 350                 355

aag aaa aac cag cat tta gct agc ttc cca ggc tgg cta gcc atg gct      1276
Lys Lys Asn Gln His Leu Ala Ser Phe Pro Gly Trp Leu Ala Met Ala
360                 365                 370                 375

cag cag aag gca gat acg gca tca gac aca aag ggc cgg caa gaa cct      1324
Gln Gln Lys Ala Asp Thr Ala Ser Asp Thr Lys Gly Arg Gln Glu Pro
                380                 385                 390

att ccc agt gat gcg gcc cag gag atg cag gag cta ggg gag aag ctt      1372
Ile Pro Ser Asp Ala Ala Gln Glu Met Gln Glu Leu Gly Glu Lys Leu
            395                 400                 405

caa gcc cta gaa agg gag aga acc aag gtc gag gag gtc aac aga cag      1420
Gln Ala Leu Glu Arg Glu Arg Thr Lys Val Glu Glu Val Asn Arg Gln
        410                 415                 420

cag agt gcc caa ctg gaa cag ctg gtc aag gag ctt cag ctg aaa gag      1468
Gln Ser Ala Gln Leu Glu Gln Leu Val Lys Glu Leu Gln Leu Lys Glu
    425                 430                 435

gat gcc cgg gcc agc ctg gag cgc ctg gtg aag gag atg gcc cca ctc      1516
Asp Ala Arg Ala Ser Leu Glu Arg Leu Val Lys Glu Met Ala Pro Leu
440                 445                 450                 455

cag gag gag ttg tct ggg aag gga cag gag gca gac cag ctc tgg cga      1564
Gln Glu Glu Leu Ser Gly Lys Gly Gln Glu Ala Asp Gln Leu Trp Arg
                460                 465                 470

cgg ctg cag gag ttg ctg gcc cac acg agc tcc tgg gag gag gag cta      1612
Arg Leu Gln Glu Leu Leu Ala His Thr Ser Ser Trp Glu Glu Glu Leu
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gca gag ttg agg cgg gag aaa                                          1633
Ala Glu Leu Arg Arg Glu Lys
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Glu Pro Ile Thr Asp Asp Ser Thr Ser Leu His Lys Ile Ser Tyr Lys
35 40 45

Leu Glu Tyr Leu Leu Gln Phe Asp Gln Lys Thr Lys Ala Thr Leu Leu
50 55 60

Gly Asn Lys Lys Asp Tyr Trp Asp Tyr Phe Cys Ala Cys Leu Ala Lys
65 70 75 80

Val Lys Gly Ala Asn Asp Gly Ile Arg Phe Val Lys Ser Ile Ser Glu
85 90 95

Leu Arg Thr Ser Leu Gly Lys Gly Arg Ala Phe Ile Arg Tyr Ser Leu
100 105 110

Val His Gln Arg Leu Ala Asp Thr Leu Gln Gln Cys Phe Met Asn Thr
115 120 125

Lys Val Thr Ser Asp Trp Tyr Tyr Ala Arg Ser Pro Phe Leu Gln Pro
130 135 140

Lys Leu Ser Ser Asp Ile Val Gly Gln Leu Tyr Glu Leu Thr Glu Val
145 150 155 160

Gln Phe Asp Leu Ala Ser Arg Gly Phe Asp Leu Asp Ala Ala Trp Pro
165 170 175

Thr Phe Ala Arg Arg Thr Leu Thr Thr Gly Ser Ser Ala Tyr Leu Trp
180 185 190

Lys Pro Pro Ser Arg Ser Ser Ser Met Ser Ser Leu Val Ser Ser Tyr
195 200 205

Leu Gln Thr Gln Glu Met Val Ser Asn Phe Asp Leu Asn Ser Pro Leu
210 215 220

Asn Asn Glu Ala Leu Glu Gly Phe Asp Glu Met Arg Leu Glu Leu Asp
225 230 235 240

Gln Leu Glu Val Arg Glu Lys Gln Leu Arg Glu Arg Met Gln Gln Leu
245 250 255

Asp Arg Glu Asn Gln Glu Leu Arg Ala Ala Val Ser Gln Gln Gly Glu
260 265 270

Gln Leu Gln Thr Glu Arg Glu Arg Gly Arg Thr Ala Ala Glu Asp Asn
275 280 285

Val Arg Leu Thr Cys Leu Val Ala Glu Leu Gln Lys Gln Trp Glu Val
290 295 300

Thr Gln Ala Thr Gln Asn Thr Val Lys Glu Leu Gln Thr Cys Leu Gln
305 310 315 320

Gly Leu Glu Leu Gly Ala Ala Glu Lys Glu Glu Asp Tyr His Thr Ala
325 330 335

Leu Arg Arg Leu Glu Ser Met Leu Gln Pro Leu Ala Gln Glu Leu Glu
340 345 350

Ala Thr Arg Asp Ser Leu Asp Lys Lys Asn Gln His Leu Ala Ser Phe
355 360 365

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Pro Gly Trp Leu Ala Met Ala Gln Gln Lys Ala Asp Thr Ala Ser Asp
    370                 375                 380

Thr Lys Gly Arg Gln Glu Pro Ile Pro Ser Asp Ala Ala Gln Glu Met
385                 390                 395                 400

Gln Glu Leu Gly Glu Lys Leu Gln Ala Leu Glu Arg Glu Arg Thr Lys
                405                 410                 415

Val Glu Glu Val Asn Arg Gln Gln Ser Ala Gln Leu Glu Gln Leu Val
            420                 425                 430

Lys Glu Leu Gln Leu Lys Glu Asp Ala Arg Ala Ser Leu Glu Arg Leu
        435                 440                 445

Val Lys Glu Met Ala Pro Leu Gln Glu Glu Leu Ser Gly Lys Gly Gln
    450                 455                 460

Glu Ala Asp Gln Leu Trp Arg Arg Leu Gln Glu Leu Leu Ala His Thr
465                 470                 475                 480

Ser Ser Trp Glu Glu Glu Leu Ala Glu Leu Arg Arg Glu Lys
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